What is claimed is:

1. A method for inferring a trait of a bovine subject from a nucleic acid sample of the bovine subject, comprising identifying in the nucleic acid sample, at least one nucleotide occurrence of at least one single nucleotide polymorphism (SNP) corresponding to position 300 of any one of SEQ ID NOS:19473 to 21982, wherein the SNP is associated with the trait, thereby inferring the trait.

2. The method of claim 1, wherein the nucleotide occurrence of at least 2 of the SNPs is determined to infer the trait.

3. The method of claim 2, wherein the nucleotide occurrences of the at least 2 SNPs comprise a haplotype allele, and wherein the method infers the trait using the identified haplotype allele.

4. The method of claim 2, wherein the at least 2 SNPs are related by dominance and/or epistasis.

5. The method of claim 4, further comprising identifying a diploid pair of haplotype alleles and inferring the trait using the diploid pair of haplotype alleles.

6. The method of claim 1, wherein the trait is marbling, tenderness, quality grade, muscle content, fat thickness, feed efficiency, red meat yield, average daily weight gain, disease resistance, disease susceptibility, feed intake, protein content, bone content, maintenance energy requirement, mature size, amino acid profile, fatty acid profile, milk production, a milk quality susceptibility to the buller syndrome, stress susceptibility and response, temperament, digestive capacity, production of calpain, caplastatin and myostatin, pattern of fat deposition, ribeye area, fertility, ovulation rate, conception rate, fertility, or susceptibility to infection with and shedding of pathogens.

7. The method of claim 6, wherein the trait is fat thickness, retail yield, tenderness, marbling, or average daily gain.

8. The method of claim 7, wherein the trait is fat thickness.

9. The method of claim 8, wherein the at least one SNP and the at least one nucleotide occurrence are selected from at least one of the SNPs and nucleotide occurrences indicated in Table 1A as associated with high fat thickness.

10. The method of claim 8, wherein the at least one SNP and the at least one nucleotide occurrence are selected from at least one of the SNPs and nucleotide occurrences indicated in Table 1A as associated with low fat thickness.

11. The method of claim 7, wherein the trait is retail yield.

12. The method of claim 11, wherein the at least one SNP and the at least one nucleotide occurrence are selected from at least one of the SNPs and nucleotide occurrences indicated in Table 1A as associated with high retail yield.

13. The method of claim 11, wherein the at least one SNP and the at least one nucleotide occurrence are selected from at least one of the SNPs and nucleotide occurrences indicated in Table 1A as associated with low retail yield.

14. The method of claim 7, wherein the trait is tenderness.

15. The method of claim 14, wherein the at least one SNP and the at least one nucleotide occurrence are selected from at least one of the SNPs and nucleotide occurrences indicated in Table 1A as associated with high tenderness.

16. The method of claim 14, wherein the at least one SNP and the at least one nucleotide occurrence are selected from at least one of the SNPs and nucleotide occurrences indicated in Table 1A as associated with low tenderness.

17. The method of claim 7, wherein the trait is marbling.

18. The method of claim 17, wherein the at least one SNP and the at least one nucleotide occurrence are selected from at least one of the SNPs and nucleotide occurrences indicated in Table 1A as associated with more abundant marbling.

19. The method of claim 17, wherein the at least one SNP and the at least one nucleotide occurrence are selected from at least one of the SNPs and nucleotide occurrences indicated in Table 1A as associated with less abundant marbling.

20. The method of claim 7, wherein the trait is average daily gain.

21. The method of claim 20, wherein the at least one SNP and the at least one nucleotide occurrence are selected from at least one of the SNPs and nucleotide occurrences indicated in Table 1A as associated with a high daily gain.

22. The method of claim 20, wherein the at least one SNP and the at least one nucleotide occurrence are selected from at least one of the SNPs and nucleotide occurrences indicated in Table 1A as associated with low daily gain.

23. A method for determining a nucleotide occurrence of a polymorphism in a bovine sample, comprising:

a) contacting a bovine polynucleotide in the sample with an oligonucleotide that binds to a target region of any one of SEQ ID NOS:24493 to 64886, wherein the target region comprises a position corresponding to position 300 of any one of

SEQ ID NOS:19473 to 21982 or wherein the target region is within 3000 nucleotides of a nucleotide corresponding to position 300 of any one of SEQ ID NOS:19473 to 21982, and

b) determining the nucleotide occurrence of a single nucleotide polymorphism (SNP) corresponding to position 300 of any one of SEQ ID NOS:19473 to 21982, wherein the determination comprises analyzing binding of the oligonucleotide or detecting an amplification product generated using the oligonucleotide, thereby determining the nucleotide occurrence of the polymorphism.

24. The method of claim 23, wherein the oligonucleotide binds to a target sequence that comprises one of the SNPs and the nucleotide occurrence is determined based on the binding of the oligonucleotide to the target sequence.

25. The method of claim 23, wherein the bovine polynucleotide is contacted with a pair of oligonucleotides that comprise a primer pair, and the nucleotide occurrence is determined using an amplification product generated using the primer pair.

26. The method of claim 23, wherein the terminal nucleotide of the oligonucleotide binds to the SNP.

27. The method of claim 25, wherein the polynucleotide is contacted with a pair of oligonucleotides each comprising a different detectable label.

28. The method of claim 27, wherein the terminal nucleotide of each oligonucleotide pair is complementary to a different nucleotide at position 300 of any one of SEQ ID NOS:19473 to 21982, or a complement thereof.

29. A method for identifying a bovine gene associated with a trait, the method comprising:

a) identifying an open reading frame present in a target region of the bovine genome, wherein the target region is located on the bovine genome less than or equal to

about 500,000 nucleotides of a single nucleotide polymorphism (SNP) corresponding to position 300 of any one of SEQ ID NOS:19473 to 21982; and

      b) analyzing the open reading frame to determine whether it affects the trait, thereby identifying a bovine gene associated with the trait.

30. The method of claim 29, wherein the trait is marbling, tenderness, quality grade, muscle content, fat thickness, feed efficiency, red meat yield, average daily weight gain, disease resistance, disease susceptibility, feed intake, protein content, bone content, maintenance energy requirement, mature size, amino acid profile, fatty acid profile, milk production, susceptibility to the buller syndrome, stress susceptibility and response, temperament, digestive capacity, production of calpain, caplastatin and myostatin, pattern of fat deposition, ribeye area, fertility, ovulation rate, conception rate, fertility, susceptibility to infection with or shedding of pathogens.

31. The method of claim 30, wherein the trait is fat thickness, retail yield, tenderness, marbling, or average daily gain.

32. The method of claim 29, wherein the target region is located within about 5000 nucleotides of a single nucleotide polymorphism (SNP) corresponding to position 300 of any one of SEQ ID NOS:19473 to 21982.

33. A method for identifying a bovine single nucleotide polymorphism (SNP) associated with a trait, comprising identifying a test SNP that is in disequilibrium with a SNP position corresponding to position 300 of one of SEQ ID NOS:19473 to 21982.

34. The method of claim 33, wherein the test SNP is in a target region of a bovine genome, wherein the target region is less than or equal to about 500,000 nucleotides from a SNP position corresponding to position 300 of one of SEQ ID NOS:19473 to 21982.

35. The method of claim 34, wherein the target region consists of at least 20 contiguous nucleotides of SEQ ID NOS:24493 to 64886.

36. The method of claim 34, wherein the target region consists of at least 20 contiguous nucleotides of SEQ ID NOS:19473 to 21982.

37. The method of claim 33, wherein the trait is marbling, tenderness, quality grade, muscle content, fat thickness, feed efficiency, red meat yield, average daily weight gain, disease resistance, disease susceptibility, feed intake, protein content, bone content, maintenance energy requirement, mature size, amino acid profile, fatty acid profile, milk production, susceptibility to the buller syndrome, stress susceptibility and response, temperament, digestive capacity, production of calpain, caplastatin and myostatin, pattern of fat deposition, ribeye area, fertility, ovulation rate, conception rate, fertility, susceptibility to infection with or shedding of pathogens.

38. The method of claim 37, wherein the trait is fat thickness, retail yield, tenderness, marbling, or average daily gain.

39. A method for sorting one or more bovine subjects, comprising:

   a) inferring a trait for a first bovine subject from a nucleic acid sample of the first bovine subject, by a method comprising identifying a nucleotide occurrence of at least one single nucleotide polymorphism (SNP) corresponding to position 300 of at least one of SEQ ID NOS:19473 to 21982, wherein the SNP is associated with the trait; and

   b) sorting the first bovine subject based on the inferred trait, and optionally repeating steps a) and b) for additional subjects, thereby sorting bovine subjects.

40. The method of claim 39, wherein the trait is marbling, tenderness, quality grade, muscle content, fat thickness, feed efficiency, red meat yield, average daily weight gain, disease resistance, disease susceptibility, feed intake, protein content, bone content, maintenance energy requirement, mature size, amino acid profile, fatty acid profile, milk

production, a milk quality, susceptibility to the buller syndrome, stress susceptibility and response, temperament, digestive capacity, production of calpain, caplastatin and myostatin, pattern of fat deposition, ribeye area, fertility, ovulation rate, conception rate, fertility, or susceptibility to infection with and shedding of pathogens, or combinations thereof.

41. The method of claim 40, wherein the trait is fat thickness, retail yield, tenderness, marbling, or average daily gain.

42. The method of claim 39, wherein the bovine subject is sorted based on at least two traits.

43. The method of claim 40, wherein at least two traits are inferred using at least one SNP.

44. The method of claim 42, wherein nucleotide occurrences of at least two SNPs are identified.

45. The method of claim 39, wherein at least two traits are inferred from nucleotide occurrences of at least three SNPs.

46. A method for selecting for breeding a bovine subject for a trait, comprising:

a) inferring a trait of a bovine candidate for use in breeding programs from a nucleic acid sample of the bovine candidate by a method comprising identifying the nucleotide occurrence of at least one single nucleotide polymorphism (SNP) corresponding to position 300 of at least one of SEQ ID NOS:19473 to 21982, wherein the SNP is associated with the trait; and

b) determining whether to select the individual for use in breeding programs based on the inferred trait, thereby selecting for breeding the bovine subject.

47. The method of claim 46, wherein the selection is implemented at the elite or breeding nucleus level or at the multiplier or foundation animal level.

48. The method of claim 46, wherein the selected bovine subject is used for breeding.

49. A bovine subject resulting from the selection and breeding according to claim 48.

50. A method for cloning a bovine subject with a desired trait, comprising:

a) identifying a nucleotide occurrence of a single nucleotide polymorphism (SNP) for the bovine subject, wherein the SNP corresponding to position 300 of one of SEQ ID NOS:19473 to 21982, and wherein the SNP is associated with the trait;

b) isolating a progenitor cell from the bovine subject; and

c) generating a cloned bovine from the progenitor cell, thereby cloning the bovine subject with the specific trait.

51. The method of claim 51, further comprising before identifying the nucleotide occurrences, determining whether the bovine subject has a desired trait.

52. The method of claim 51, wherein the SNP affects the trait.

53. A bovine subject resulting from the cloning of claim 50.

54. The method of claim 50, wherein nucleotide occurrences of at least two single nucleotide polymorphisms (SNPs) corresponding to position 300 of any one of SEQ ID NOS:19473 to 21982, are identified and used to clone the bovine subject.

55. The method of claim 50, further comprising before identifying the nucleotide occurrences, identifying a trait of the bovine subject, wherein the bovine subject has a desired trait and wherein the at least two SNPs affect the trait.

56. The method of claim 50, wherein the bovine subject is a female.

57. The method of claim 56, wherein the progenitor cell is an ovum.

58. An embryo produced by the method of claim 50.

59. A method of tracking meat of a bovine subject, comprising:

a) identifying nucleotide occurrences for more than one genetic markers of the bovine subject;

b) identifying the nucleotide occurrences for the more than one genetic markers for a meat sample; and

c) determining whether the nucleotide occurrences of the bovine subject are the same as the nucleotide occurrences of the meat sample, wherein identical nucleotide occurrences indicate that the meat sample is from the bovine subject, thereby tracking meat from the bovine subject.

60. The method of claim 59, wherein the more than one genetic markers comprise at least three single nucleotide polymorphisms (SNPs).

61. The method of claim 59, wherein the method further comprises

d) determining whether the meat originated from the bovine subject using another tracking method.

62. The method of 61, further comprising comparing the results of step c) and step d).

63. The method of claim 60, wherein nucleotide occurrences for at least 5 SNPs are identified.

64. The method of claim 60, wherein nucleotide occurrences for at least 300 SNPs are identified.

65. The method of claim 59, wherein the nucleotide occurrence data for the bovine subject is stored in a computer readable form.

66. The method of claim 65, wherein the computer readable form is a database.

67. The method of claim 60, wherein the at least one SNP comprises at least one SNP corresponding to position 300 of one of SEQ ID NOS:19473 to 21982.

68. A method for establishing the economic value of a bovine subject, comprising
a) inferring a trait of the bovine subject from a nucleic acid sample of the bovine subject by a method comprising identifying nucleotide occurrences for at least one single nucleotide polymorphism (SNP) corresponding to position 300 of at least one of SEQ ID NOS:19473 to 21982, wherein the SNP is associated with the trait; and
b) determining the value of the bovine subject, wherein the trait affects the value determination, thereby establishing the economic value of the bovine subject.

69. The method of claim 68, further comprising using traditional factors affecting economic value and the inference to establish the economic value of the bovine subject.

70. A method for improving profits related to selling beef from a bovine subject, the method comprising:
a) inferring a trait of the bovine subject from a nucleic acid sample of the bovine subject by a method comprising identifying a nucleotide occurrence for at least one single nucleotide polymorphism (SNP) corresponding to position 300 of at least one of

SEQ ID NOS:19473 to 21982, wherein the SNP is associated with the trait; and wherein the trait affects the value of the beef; and

b) using the inference to affect management or selection of the subject, or to affect a chain of commerce of the product or the subject, thereby improving profits related to selling the product.

71. The method of claim 70, wherein the inference affects the management of at least one of food intake, diet composition, administration of feed additives or pharmacological treatments such as vaccines, antibiotics, hormones and other metabolic modifiers, age and weight at which diet changes or pharmacological treatments are imposed, days fed specific diets, castration, feeding methods and management, imposition of internal or external measurements and environment of the bovine subject based on the inferred trait.

72. The method of claim 71, wherein the trait comprises pleitropic effects and non-additive genetic effects.

73. The method of claim 72, wherein the meat is obtained at a time point that is affected by one or more of an inferred trait and the food intake, diet composition and management of the bovine subject.

74. The method of claim 73, wherein the chain of commerce is affected by sorting the meat based on the inferred trait.

75. A computer system comprising:
a) a database having records containing information regarding the relationship between nucleotide occurrences of at least two bovine single nucleotide polymorphisms (SNPs) and a trait of one or more traits, wherein the at least two SNPs correspond to any two of position 300 of SEQ ID NOS:19473 to 21982; and

b) a user interface allowing a user to input nucleotide occurrence data for the at least two bovine SNPs for a bovine subject to be used to query the database, and displaying results of the query.

76. The computer system of claim 75, wherein the records include descriptive information from an external database that correlates the biomolecular sequences to records in the external database.

77. The computer system of claim 75, wherein the database comprises records representing a bovine SNP map comprising at least 3000 SNPs.

78. The computer system of claim 75, wherein the computer system is a handheld device.

79. A method for using a computer system to present information pertaining to a plurality of records containing information regarding the relationship between nucleotide occurrences of at least two bovine single nucleotide polymorphisms (SNPs) and one or more traits, the method comprising

a) providing a user interface for inputting nucleotide occurrences of the at least two bovine SNPs for a bovine subject, wherein the at least two bovine SNPs comprise at least two SNPs corresponding to position 300 of one of SEQ ID NOS:19473 to 21982, wherein the at least two SNPs is associated with the one or more traits;

b) locating data corresponding to the entered query information; and

c) displaying the data corresponding to the entered query information.

80. The method of claim 79, wherein the plurality of records represent a bovine SNP map comprising at least 3000 SNPs.

81. A computer system comprising:

a) a database having records containing information regarding at least two bovine single nucleotide polymorphisms (SNPs) corresponding to position 300 of SEQ ID NOS:19473 to 21982; and

b) a user interface allowing a user to input nucleotide occurrences of the at least two bovine SNPs for a bovine subject to be used to query the database and display results of the query.

82. The computer system of claim 81, wherein the database comprises records representing a bovine SNP map comprising at least 3000 SNPs.

83. The computer system of claim 81, wherein the computer system is a handheld device.

84. The computer system of claim 81, wherein the records comprise information regarding one or more traits associated with the at least two bovine SNPs.

85. A computer program comprising a computer-usable medium having computer-readable program code embodied thereon comprising a plurality of sequence records stored in a database, the sequence records containing information regarding the relationship between a trait and nucleotide occurrences of at least three bovine single nucleotide polymorphisms (SNPs) comprising at least two SNPs corresponding to position 300 of SEQ ID NOS:19473 to 21982, wherein the SNP is associated with the trait; the computer program product comprising computer-readable program code for effecting the following steps within a computing system:

a) providing a user interface capable of allowing a user to input nucleotide occurrences of the at least three bovine SNPs for a bovine subject;

b) locating data corresponding to the entered query information; and

c) displaying the data corresponding to the entered query.

86. The computer program product of claim 85, wherein the database comprises records representing a bovine SNP map comprising at least 3000 SNPs.

87. A method for maximizing a physical characteristic of a bovine subject, the method comprising:

a) inferring a trait of the bovine subject from a nucleic acid sample of the bovine subject by a method comprising identifying in the sample a nucleotide occurrence for a single nucleotide polymorphism (SNP) corresponding to position 300 of one of SEQ ID NOS:19473 to 21982, wherein the SNP is associated with the trait, and wherein the trait affects the physical characteristic; and

b) using the inferred trait to affect management of at least one of food intake, diet composition, administration of feed additives or pharmacological treatments such as vaccines, antibiotics, hormones and other metabolic modifiers, age and weight at which diet changes or pharmacological treatments are imposed, days fed specific diets, castration, feeding methods and management, imposition of internal or external measurements or environment of the bovine subject based on the inferred trait.

88. A kit for determining nucleotide occurrences or haplotype alleles of bovine SNPs, comprising an oligonucleotide probe, primer, or primer pair, or combinations thereof, for identifying the nucleotide occurrence of at least one bovine single nucleotide polymorphism (SNP) corresponding to position 300 of SEQ ID NOS:19473 to 21982, wherein the SNP is associated with the trait.

89. The kit of claim 88, further comprising one or more detectable labels.

90. The kit of claim 88, wherein the kit comprises a plurality of oligonucleotide probes, primers, or primer pairs, or combinations thereof, for identifying the nucleotide occurrence of at least two of the SNPs.

91. The kit of claim 88, wherein the kit comprises at least two probes, primers, or primer pairs for identifying the nucleotide occurrence of at least two SNPs that comprise a haplotype, and wherein the kit allows a determination of a haplotype allele that is associated with the trait.

92. A method for creating a progeny bovine subject, the method comprising:

a) inferring a trait for a first bovine subject from a nucleic acid sample of the first bovine subject, by a method comprising identifying the nucleotide occurrence of at least one single nucleotide polymorphism (SNP) corresponding to position 300 of one of SEQ ID NOS:19473 to 21982, wherein the SNP is associated with the trait;

b) selecting the first bovine subject based on the inferred trait; and

c) mating the first bovine subject and a second bovine subject, thereby creating the progeny bovine subject.

93. The method of claim 92, wherein the second bovine subject is selected based on having the same or a complementary inferred trait inferred by at least one of the SNPs.

94. The method of claim 92, wherein the inferred trait is marbling, tenderness, quality grade, muscle content, fat thickness, feed efficiency, red meat yield, average daily weight gain, disease resistance, disease susceptibility, feed intake, protein content, bone content, maintenance energy requirement, mature size, amino acid profile, fatty acid profile, milk production, a milk quality susceptibility to the buller syndrome, stress susceptibility and response, temperament, digestive capacity, production of calpain, caplastatin and myostatin, pattern of fat deposition, ribeye area, fertility, ovulation rate, conception rate, fertility, or susceptibility to infection with and shedding of pathogens.

95. The method of claim 94, wherein the trait is fat thickness, retail yield, tenderness, marbling, or average daily gain.

96. The method of claim 95, wherein the trait is fat thickness.

97. The method of claim 95, wherein the trait is average daily gain.

98. A method for identifying a target bovine polynucleotide affecting a trait, comprising:

A) providing a polynucleotide derived from a bovine subject, or sequence information thereof; and

B) determining whether the polynucleotide is at least 90% identical to a SNP-containing polynucleotide by comparing the polynucleotide or the sequence information provided in A) to a polynucleotide consisting essentially of:

a) a polynucleotide according to any one of SEQ ID NOS:19473 to 21982,

b) a contiguous fragment of a polynucleotide according to any one of SEQ ID NOS:24493 to 64886 that is at least 300 nucleotides in length and that comprises a single nucleotide polymorphism corresponding to position 300 of one of SEQ ID NOS:19473 to 21982, wherein the polymorphism is associated with the trait; or

c) a complement of a) or b);

wherein a polynucleotide or sequence thereof that is at least 90% identical to the SNP-containing polynucleotide identifies the bovine polynucleotide as a target polynucleotide for the trait.

99. The method of claim 98, wherein the polynucleotide derived from a bovine subject comprises bovine genomic sequences.

100. An isolated polynucleotide identified according to the method of claim 98.